



## **Outcome of EPIZONE Extension ON VER/VNN: Pathogenicity study of 10 betanodavirus strains with an in vivo challenge in European sea bass (*Dicentrarchus labrax*)**

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# **OUTCOME OF EPIZONE Extension ON VER/VNN: Pathogenicity study of 10 betanodavirus strains with an *in vivo* challenge in European sea bass (*Dicentrarchus labrax*)**

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## **Abstract:**

Viral encephalopathy and retinopathy (VER) otherwise known as viral nervous necrosis (VNN) is a severe pathological condition, caused by small RNA viruses belonging to the Nodaviridae family, genus Betanodavirus. The disease, which has been described in more than 45 fish species worldwide, is considered the most serious viral threat affecting marine farmed species in the Mediterranean region, thus representing one of the bottlenecks for further development of aquaculture industry.

Epidemiological investigations carried out in different geographical areas demonstrated that Betanodavirus can be detected in wild fish as well as other aquatic organisms (artemia, rotifers, molluscs and crustaceans) in addition to farmed fish.

The RGNNV genotype is the most widespread in the Mediterranean region, nevertheless some strains, characterized by containing genetic material belonging to both the RGNNV and the SJNNV genotypes in their genome, have been identified too. The existence and the spread of these genetically different viral agents that share inter-genotype genetic material could be one of the major causes that characterize the differences in mortality observed in the field.

In order to contribute to a better understanding of the pathogenicity of circulating viruses, ten selected VER/VNN strains differing for origin and/or genotype were tested “*in vivo*” by challenging sea bass juveniles in infection trials. The infection was performed under controlled conditions and all the infected groups were monitored for 68 days after infection. The results clearly confirmed the pathogenicity, to different degrees, of all the selected strains, including one strain belonging to SJNNV genotype and four reassortant strains from SJNNV and RGNNV genotypes and underlined the potential risk represented by sea bream and other apparently resistant species in the transmission of the disease to other highly susceptible species.